GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

July 24, 2002, 11:24:03; Search time 95.25 Seconds

294.716 Million cell updates/sec

Run on:

1 MAMDSSLQARLFPGLAIKIQ.... PCT-US02-13994-20 3685 .LAMQLEEQASRQISSKKRPQ 725

Scoring table: BLOSUM62 Sequence: Title: Perfect score:

Gapop 10.0 , Gapext 0.5

105224 seqs, 38719550 residues

Total number of hits satisfying chosen parameters:

105224

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database : SwissProt_40:*

Fred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total acore distribution.

					SUMMAKIES	
Result		Query				
₹	Score	Match	Length	DB	ID	Description
1	3683	99.9	725	<u>.</u> ا	MCAK HUMAN	
N	3252	88.2	718	,	MCAK_CRIGR	P70096 Cricetulus
w	2856		671	_	KRP2_RAT	_
-	2361	64.1	730	_	RCM1_XENLA	
	1868.5	50.7	679	-	KIF2_HUMAN	homo sar
10	1859	50.4	716	_	KIF2_MOUSE	_
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18	509.5	13.8	701	_	KE3A MOUSE	
19	506	13.7	1060	۳	EG51_XENLA	P28025 xenopus lae
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Homo sapiens (Human). Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Primates; Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.

MEDLINE-98094213; PubMed-9434124; IISSUE=T-cell; SEQUENCE FROM N.A. NCBI_TaxID-9606; Sohn U., Kim Y.H.;

Biochim. Biophys. Acta 1359:181-186(1997). gene Kim I.-G., Jun D.Y., Cloning and expression of human mitotic centromere-associated kinesin

SEQUENCE FROM N.A.

rissue-Kidney, and Uterus;

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CC BRAIN LUNG, LUTER, SKELETAL MISCLE, KIDNEY, OR PANCIES.

CC -1- SIMILARITY, BELONGS TO THE KINESIN-LIKE PROTEIN FAMILY, MCAR/KIF?

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EMBL; U63743; AAC27660.1; -EMBL; BC011924, AAH11924.1; -EMBL; BC008764; AAH08764.1; -EMBL; BC008764; AAH08764.1; -HSSP; P17119; 3KAR.
MIN; 604538; --

Interpro; IPR001752; kinesin.
Pfam; PF00225; kinesin; 2.
PRINTS; PR00380; KINESINHEAVY.
SMART; SN00129; KISC; 1.

PROSITE; PS00411; KINESIN_MOTOR_DOMAIN1; 1.

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DOMAIN 253
DOMAIN 253
DOMAIN 619
DOMAIN 696
NP_BIND 348
DOMAIN 415
CONFLICT 449
CONFLICT 698
SEQUENCE 725 NA
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Motor protein; Microtubules; ATP-binding; Colled coil;
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                                                       DWLELSENTEQPDYDLETFYNKAESALAQQAKHFSALRDVIKALRLAMQLEEQASRQISS
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ATP (POTENTIAL).

NUCLEAR LOCALIZATION SIGNAL (
I -> L (IN REF. 1).

R -> P (IN REF. 2). AAA(08764).
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Pred. No. 1
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KINESIN-MOTOR (BY SI
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-> P (IN REF. 2; AAH087
5BDECC133AB4B55C CRC64;
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MCAK_CRIGR
P70096;
01-NOV-1997
30-MAY-2000
01-MAR-2002
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1- FUNCTION: PRESENT THROUGHOUT THE CELL CYCLE, ASSOCIATES WITH

CENTROMERES AT EARLY PROPHASE. AND REMAINS ASSOCIATED WITH THE

CENTROMERE UNTIL AFTER TELOPHASE.

1- SUBCELLULAR LOCATION: Cytoplasmic and nuclear.

1- SIMILARITY: BELONGS TO THE KINESIN-LIKE PROTEIN FAMILY. MCAK/KIF2
DOMAIN
NP_BIND
DOMAIN
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "identification and partial characterization of mitotic centromere-
associated kinesin, a kinesin related protein that associates with
centromeres during mitosis.";
J. Cell Biol. 128:95-105(1995).
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                                                                                                      Motor protein; Microtubules;
Nuclear protein.
                                                                                                                                 PROSITE; PS00411; KINESIN_MOTOR_DOMAIN1; 1.
PROSITE; PS50067; KINESIN_MOTOR_DOMAIN2; 1.
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Pfam; PF00225; kinesin; 2.
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2000 (Rel. 39, Last asquence update)
2002 (Rel. 41, Last anotaxion update)
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88.5%;
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4; Mismatches 4
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KAL Cell BAL 18638-6547(1998),

BABL ME120931 AAD56597 1 TOTRED

BABL ME120988 AAD56597 1 TOTRED

BABL ME120989 AAD56597 1 TOTRED

BABL ME120989 AAD56597 1 TOTRED

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BABL ME120991 AAD56597 1 TOTRED

PERSON PROTEINS MED 1 TOTRED

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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JNJ-2001 (TREMBLrel. 17, Last annotation update)
METHYL-CPG BINDING PROTEIN 2.
                                                                                  09Z2E1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pfam; PF01429; MBD; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hendrich B., Abbott C., McGueen H., Chambers D., Cross S., Bird A.; 
"Genomic structure and chromosomal mapping of the murine and human mbdl, mbd2, mbd3, and mbd4 genes."; 
Mamm. Genome 10:906-912(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A. MEDLINE-99373255; PubMed-10441743;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Identification and characterization of a family of mammalian methyl-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                dendrich
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A. 
MEDLINE-98449942; PubHed-9774669;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                181 AADTEEMDIEMDSGDEA 197
                                                                                                                                                                                                                                                                                                                                                       335 PITGQVSAAVEKNPAVWLNTSQPLCKAFIVTDEDIRKQEERVQQVRKKLEEALMADILSR 394
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                                                                                                                                                                                                                                         395 AADTEEMDIEMOSGDEA 411
                                                                                                                                                                                                                                                                                                                                                                                                                   121 PITGQVSAAVEKNPAVWLNTSQPLCKAFIVTDEDIRKQEERVQQVRKKLEEALMADILSR 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              215 PSKLQKNKQRLRNDPLNQNKGKPDLNTTLPIRQTASIFKQPVTKVTNHPSNKVKSDPQRN 274
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61 NEOPROLEWEKKLOGLSASDVTEOIIKTMELPKGLOGVGPGSNDETLLSAVASALHTSSA 120
عر
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 PSKLQKNKQRLRNDFLNONKGKPDLNTTLPIRQTASIFKQPVTKVTNHPSNKVKSDPQRM 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NEOPROLFWEKRLOGLSASDVTEQIIKTMELPKGLOGVGPGSNDETLLSAVASALHTSSA 334
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 411 AA;
                                                                             PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             43254 MW; FC4E5E0CF9BA0FFA CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Chordata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 100.0%; Score 998; DB 4;
100.0%; Pred. No. 2.6e-76;
tive 0; Mismatches 0;
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                                                                             PRT;
                                                                             11 2
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EMBL: AF120986; AAD5072.1:

EMBL: AF120983: AAD5072.1:

EMBL: AF120983: AAD5072.1:

EMBL: AF120985: AAD5072.1:

EMBL: AF120985: AD5072.1:

EMBL: AF120985:
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01-MAY-1999 (TERMELTel. 10, Last sequence update)
01-JUN-2001 (TERMELTel. 17, Last annotation update)
                                                                                           Renopus laevis (African clawed frog);
Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibla; Butrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
Xenopodinae; Xenopus.
                                                                                                                                                                                                                                                  0990M9;
01-MAY-2000 (TIEMSLIFE), 13, Created)
01-MAY-2000 (TIEMSLIFE), 13, Last sequence update)
01-WAY-2000 (TIEMSLIFE), 13, Last annotation update)
METHIC-OPG SINDING PROTEIN MEDJ.
                                                                                                                                                                                                                                                                                                                                                                                                                   Q9PUM9
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"Identification and characterization of a family of mammalian methyl-
CpG binding proteins:";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hendrich B., Abbott C., McQueen H., Chambers D., Cross S., Bird A.; 
"Genomic structure and chromosomal mapping of the murine and human mbdl, mbd2, mbd3, and mbd4 genes."; 
Mamm. Genome 10:906-912(1999).
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MEDLINE-98449942;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mus musculus (Mouse)
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                                                                NCBI_TaxID-8355;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mol. Cell. Biol. 18:6538-6547(1998).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          398 AADTEEVDIDMDSGDEA 414
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     181 AADTEENDIEMDSGDEA 197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 338 PITGOVSAAVEKNPAVWLNTSOPLCKAFIVTDEDIRKGEERVOOVRKKLEEALMADILSR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        121 PITCQVSAAVEKNPAVWLNTSQPLCKAFIVTDEDIRKQEERVQQVRKKLEEALMADILSR 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   278 NEOPROLFWEKRLOGLSASDVTEQIIKTMELPKGLOGVGPGSNDETLLSAVASALHTSSA 337
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    218 PSKLQKNKQRLRNDPLNQNKGKPDLNTTLPIRQTASIFKQPVTKFTNHPSNKVKSDPQRM 277
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                   PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           98.8%; Score 986; DB 11; 98.5%; Pred. No. 2.7e-75;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           9601D95E347E8E53 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                              282 AA.
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Database
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 2000000000
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Perfect score:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SPTREMBL_19:*
1: sp_archea:*
2: sp_bacteria:*
3: sp_fung1:*
4: sp_human:*
                                                                                                                                                                                                                               13:
10:
13:
13:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               562222 seqs, 172994929 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gapop 10.0 , Gapext 0.5
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Copyright (c) 1993 - 2000 Compugen Ltd.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          sp_mammal: *
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     sp_invertebrate:*
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Pred. Mo. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Regult No.	Score	Query	Query Match Length DB	B	ID	Description
. :				i		
	1528	99.5	424	•	000312	000312 homo sapien
2	1497.5	97.5	465	_	Q9BUB5	09bub5 homo sapien
w	1436	93.5	415	Ξ	008605	008605 mus musculu
_	1258.5	81.9	422	<u>.</u>	Q9YGW0	Ogvow0 xenopus lae
5	1125.5	73.3	465	•	Q9нвн9	09hbh9 homo sanien
6	1125.5	73.3	472	4	Q9Y2N6	09v2n6 homo sapien
7	1116	72.7	412	H	008606	008606 mus musculu
8	984	64.1	316	•	Q9NT28	Q9nt28 homo sapien
9	984	64.1	414	•	О9нвн8	09hbh8 homo sapien
10	186	63.9	414	•	Q9UHRO	Q9uhr0 homo sapien
11	756.5	49.3	1090	u	Q9VGI5	09vq15 drosophila
12	756.5	49.3	1142	G,	Q9VGI4	09vq14 drosoph11a
13	751.5	48.9	1150	U	Q9454B	094548 drosophila
14	715	46.5	206	11	Q9D893	09d893 mus musculu
15	601	39.1	158	_	98VN60	Ognv89 homo sanien
16	596.5	38.8	761	S	022005	022005 caenorhabdi

5	4	(Li	2	1	0	39	8	37	36	S	34	33	32	31	30	29	28	27	26	25	24	23	22	21	20	19	18	17
358.5	360	360	360.5	360.5	361	365	365	365	365.5	365.5	365.5	366	368	369	369	376	377	377.5	379	381	382	388.5	388.5	399	400	01	403	417
23.3	23.4	23.4	23.5	23.5	23.5		23.8	23.8	23.8	23.8	23.8	23.8	24.0	24.0	24.0	24.5	24.5	24.6	24.7	24.8	24.9	25.3	25.3		26.0	26.1	26.2	27.1
573	773	773	520	518	554	481	476	460	646	477	309	772	802	531	531	493	350	190	737	735	471	473	156	733	382	758	733	208
10	:	11	10	10	10	-	•	-	10	H	H	-	-	10	10	u	ر.	10	13	-	-	=	-	=	-	ďп	-	1
P93838	Q91X18	Q9Z2B9	Q9SJ61	Q9AXA7	049717	Q9Y3J7	096NX5	095523	Q38870	Q91VB2	008763	075676	075582	094900	Q9ZSA2	015872	025108	042396	Q9PTN1	Q96C05	060491	054992	Q9BVX9	Q9D2C0	016644	Q9BE29	Q96J38	Q9CWH9
cuc		Q9z2b9 mus musculu			٦,			=			w		075582 homo sapien		N	015872 paramecium	Q25108 hemicentrot		xen		8	anus	9	D mus		Q9be29 macaca fasc	DINO DINO	Q9cwh9 mus musculu

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InterPro: IMPRODOZOG: Ser Lb_PXINASE.
InterPro: IMPRODOZOG: Ser Lb_PXINASE.
Pfam: PF00055; PKINASE.
SMART: SM00120: S_TKc: 1.
SMART: SM00120: TyKrc: 1.
SMART: SM00120: TyKrc: 1.
SMART: SM00120: TyKrc: 1.
SMART: SM00107: PROTEIN_KINASE_DAY: UNKNOWN_1.
PROSITE: PS00107: PROTEIN_KINASE_DAY: 1.
ATP-DAINGING: PROTEIN_KINASE_DAY: 1.
ATP-DAINGING: PROTEIN_KINASE_ST: 1.
ATP-DAINGING: KINASE, ST: 1.
ATP-DAINGING: KINASE, 
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01-JUN-2001 (TERMILTO]. 17. Last sequence update)
01-DEC-2001 (TERMILTO]. 17. Last sequence update)
SIMILAR TO MAR KINASE THERACTING SERVINE/THREWITER KINASE 1.
Hono appiens (Ruman). THERACTING SERVINE/THREWITER KINASE 1.
EDWARTYOTA (METAZOS: OFFICATES). Craniata: Vertebrata: Euteleostomi;
Mammalia; Eutheria: Primates; Catairhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Q9BUB5;
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200 QGQAPEKGLPTPQVLQRNSSTMDLTLFAAEAIALNRQLSQHEENELAEEPEALADGLCSM 259
                                                                                                                                                                                                                                                                                                                                                                                                         195 PTSASQVAGTTGIAHRDLKPENILCESPEKVSPVKICDFDLGSGMKLNNSCTPITTPELT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     135 HIOKOKHENEREASRYVKDVAAALDELHTKDKVSLCHLGWSAMAPSGLTAAPTSLGSSDP 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         375
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                                                                                                                                                                                                                                                                                     80 TPCGSAEYMAPEVVEVFTDQATFYDKRCDLMSLGVVLVIMLSGYPPFVGHCGADCGWDRG 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity 87.0 hes 288; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 ------GIAHRDLKPENILCESPEKVSPVKICDFDLGSGMKLNNSCTPITTPELT 79
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                                                                                                                         EVCRVCQNKLFESIQEGKYEFPDKDWAHISSEAKDLISKLLVRDAKQKLSAAQVLQHPWV 199
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           97.5%; Score 1497.5; DB 4; Length 465; B7.0%; Pred. No. 8.2e-133; Indels 41;
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Best Local S
Matches 269
Q9YGWO PRELIMINARY;
Q9YGWO;
01-MAY-1999 (TIEMBLITEL: 10,
                                                                                                                                                                                                                                                                                                                                                                                                                           Mus musculus (Mouse).
Eukaryota: Metazoa: Chordata: Craniata: Vertebrata: Euteleostomi:
Mammalia: Eutheria: Rodentia: Sciurognathi: Muridae; Murinae: Mus
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01-JUL-1997 (TIEMBLIEL 04, Las
01-DEC-2001 (TIEMBLIEL 19, Las
MAP KINASE INTERACTING KINASE.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDIINE-97299868; PubMed-9155017;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
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- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES
                                                                                            363 EENELAEEQEALAEGLCSMKLSPPSKSRLARRRALAQAGRSRDANP
                                                                                                                                                           181 VRDAKQKLSAAQVLOHPWVQGQAPEKGLPTPQVLQRNSSTMDLTLFAAEAIALNRQLSQH 240
                                                                                                                                                                                                        243
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                                                                                                                                                                                                                                                                                                         123 HIOKRKHFNEREASRVVRDVATALDFLHTKGIAHRDLKPENILCESPEKVSPVKICDFDL 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       260 KLSPPCKSRLARRRALAQAGRGENRSPPTAL 290
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61
                                                                                                                                                                                                                                                                                                                                                                               Local Similarity
                                                                                                                                                                                                                                                                                                                                  1 HIQKQKHFNEREASRVVRDVAAALDFLHTKGIAHRDLKPENILCESPEKVSPVKICDFDL 60
                                                                                                                       EENELAEEPEALADGLCSMKLSPPCKSRLARRALAQAGRGENRSP 286
                                                                                                                                              VRDAKORLSAAQVLOHPWVQGQAPERGLPTPQVLQRNSSTMDLTLFAAEAIALNRQLSQH
                                                                                                                                                                                                 SGYPPFVGHCGADCGWDRGEVCRWCQNKLFESIQEGKYEFPDKDWAHISNEAKDLISKLL
                                                                                                                                                                                                                SGYPPFVGHCGADCGWDRGEVCRVCQNKLFESIGEGKYEFPDKDWAHISSEAKDLISKLL 180
                                                                                                                                                                                                                                                    GSGVKLNNSCTPITTPELTTPCGSAEYMAPEVVEVFRDEATFYDKRCDLWSLGVVLYIML
                                                                                                                                                                                                                                                                               GSGMKLNNSCTPITTPELTTPCGSAEYMAPEVVEVFTDQATFYDKRCDLMSLGVVLYIML
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(TremBirel. 04, Last sequence update)
(TremBirel. 19, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                    Conservative
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Copyright (c) 1993 - 2000 Compugen Ltd.
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ALIGNMENTS

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AAY07092 standard; Protein; 897 AA.

AAY07092;

02-JUL-1999

(first entry)

Colon cancer associated antigen precursor sequence

prostate cancer. Cancer associated antigen; diagnosis; research; treatment; human; breast cancer; colon cancer; gastric cancer; renal cancer; lung cancer;

Homo sapiens

W09904265-A2

28-JAN-1999.

22-JUN-1998; 17-JUL-1997; 10-OCT-1997; 10-OCT-1997; 10-OCT-1997; 11-OCT-1997; 15-JUL-1998; 98US-0102322. 97US-0896164. 97US-0061599. 97US-0061765. 97US-0948705. 97US-0921697. 98WO-US14679

(LUDW-) LUDWIG INST CANCER RES.

Tureci 0; Chen Y, Gout I, Pfreundschuh M, Chen Y, Gure A, Sahin U, O'Hare M, I Obata Y, Old LJ; I, Stockert E;

WPI; 1999-132448/11

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Best Local Simi
Matches 896;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Disclosure: Page 652-654; 787pp; English
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                  DTVWNEMHSSSAVRMAVGCLLELAFKVAAGELKNGFAIIRPPGHHAEESTAMGFCFFNSV
                                                                      RIRGRKATLDEIQTVHSEYHTLLYGTSPLNRQKLDSKKLLGPISQKMYAVLPCGGIGVDS
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05-APR-1999;
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ACC7446 to AAC77606 encode the proteins given in AAB40237 to AAB43397 which represent the human ORFX open reading frames 1 to 3161. The ORFX sequences have activities such as: cytostatic; hepatotropic; vulnerary.

Novel nucleic acids and peptides derived from open reading useful for treating e.g. cancers, proliferative disorders,

neurodegenerative disorders and cardiovascular disease

Claim 11; Page 4728-4731; 5507pp; English

N-PSDB;

2000-602362/57. DB; AAC77217.

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OM protein - protein search, using sw model
                                                                                      GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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Searched:	Scoring table:	Title: Perfect score: Sequence:	Run on:
747574 segs, 111073796 residues	BLOSUM62 Gapop 10.0 , Gapext 0.5	PCT-US02-13994-21 3941 1 RVKATLSERKIGDSCDKDLPEASTIMVYQIIFQMYRTPTL 752	July 24, 2002, 11:10:51 ; Search time 345.34 Seconds (without alignments) 241.172 Million cell updates/sec

Minimum DB seq length: 0
Maximum DB seq length: 200000000 Total number of hits satisfying chosen parameters:

Post-processing: Minimum Match 01 Maximum Match 100%

A_Geneseq_032802:*

| SIDSI/gcqdata/hold-geneseq/geneseqp-embl/AA1981_DAT:*
| SIDSI/gcqdata/hold-geneseq/geneseqp-embl/AA1981_DAT:* Listing first 45 summaries

RESULT AAY07108

,

AAY07108 standard; Protein; 752 NA

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.

Result No.	Score	Query Match	Query Match Length DB	DB	ID	Description
_	3941	100.0	752	20	AAY07108	Colon cancer assoc
2	2197	55.7	682	22	ABG23259	Novel human diagno
3	328.5	8 	2515	22	ABB64427	Drosophila melanog
-	273.5	5.9	777	22	AAU07898	Polypeptide sequen
u	268	6.8	928	22	AAU07880	Polypeptide sequen
5	191.5	4.9	1098	22	AAU03596	Human 140kDa Shc a
7	176	. 51	579	21	AAB41958	Human ORFX ORF1722
œ	166	4.2	3248	17	AAR99795	Kinetochore protei
9	165	4.2	2482	16	AAR72826	Human mitosin, Ho
10	165	4.2	2482	19	AAW23996	Human mitosin amin
11	160.5	4.1	633	22	AAB93452	Human protein sequ

Arabidopsis thalia		2	1703	3.2	126.5	5
Cellulose synthase		N	1124	3.2	126.5	4
S. cerevisiae DNA	2 AAB46722	N	745	J. 2	127	3
Human HulfRG-1 pro		N	468	3.2	127	2
Drosophila melanog	2 ABB65616	N	2271	<u>ن</u> د	127.5	
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Drosophila melanog	2 ABB58717	'n	1049	س س	129	39
Novel human diagno	2 ABG20656	N	391	ω 	129	38
Human polypeptide		N	864	ω ω	129.5	37
Drosophila melanog		N	3263	ω	130	36
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Human WRN gene pro	8 AAY14517	=	1432		131.5	3
Plasmodium falcipa		N	1979	ن ن	132	32
Human SCP-1 mutein	2 AAG66581	ĸ	976	ω .ω	132	31
P. falciparum live		1	1786	3. •	132.5	30
H. pylori GHPO 175		19	1743	3. •	132.5	29
Staphylococcus aur		2	3158	3.4	133	28
Human ORFX ORF1356		2	2096	3.4	133	27
Staphylococcus aur	2 AAU34207	2	2025	ω •	133	26
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Novel human diagno	_	2	944		138	16
Drosophila melanog		2	1543		139	5
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TD.	_	2	1019		141	<u>_</u>
Drosophila melanog	2 ABB62874	22	926	3.7	146.5	2

ALIGNMENTS

Colon cancer	02-JUL-1999	AAY07108;
Colon cancer associated antigen precursor sequence.	02-JUL-1999 (first entry)	
precursor		
 sequence.		

Cancer associated antigen; diagnosis; research; treatment; human; breast cancer; colon cancer; gastric cancer; renal cancer; lung cancer; prostate cancer.

PRESENTATION OF THE PRESEN 22-JUN-1998; 17-JUL-1997; 10-OCT-1997; 10-OCT-1997; 10-OCT-1997; (LUDW-) LUDWIG INST CANCER RES 11-OCT-1997; 15-JUL-1998; 28-JAN-1999. W09904265-A2 Homo sapiens. 98US-0102322. 97US-0896164. 97US-0061599. 97US-0061765. 97US-0948705. 97GB-0021697. Sahin U, 98WO-US14679 O'Hare M, ' Obata Y,

Chen Y, Gout I, Pfreundschuh M, Turecl O; Stockert E; 01d LJ

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New isolated cancer associated nucleic acids and polypeptides -
isolated using sers from cancer patients, used to develop products
for the diagnosis, monitoring or treatment of cancers
                                                                                                                                                                 WPI; 1999-132448/11
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Disclosure; Page 678-680; 787pp; English.

binds to the NAM, an expression product or a fragment of an expression product complexed with an HLA molecule; and (b) determining the Interaction between the agent and the NAM or the expression product as a determination of the disorder. The products and methods can be used in the dispnosis, monitoring, research, or treatment of conditions on the characterised by the expression of various canner associated antigens. The invention provides nucleic acid sequences and encoded polypeptides which are canner associated antigen precursors expressed in human breast which are canner associated antigen precursors expressed in human breast cancer regal cancer, colon cancer, gastic cancer, protathe cancer and tonce of the cancer and cancer. The invention relates to a method for diagnosing a disorder characterised by expression of a human cancer associated antigen precursor coded for by expression of a human cancer associated antigen precursor coded for by expression of a human cancer method comprises; (a) contacting a biological sample isolated from a subject with an agent that specifically lung cancer.

Sequence 752 AA;

Similarity

100.0%; Score 3941; 100.0%; Pred. No. 0;

DB 20;

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Query Match
Best Local S
Matches 752
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New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess biodiversity
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                                                                                                                                                                                                                                                Claim 20; SEQ ID No 53618; 103pp; English
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23-AUG-2000;
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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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OM protein protein search, using sw model

Run on: July 24, 2002, 11:11:01; Search time 346.34 Seconds tithout alignments) 63.179 Hillion cell updates/sec

Title: Perfect score: Sequence: PCT-US02-13994-23 998 1 PS#1~~ PSKLOKNKQRLRNDPLNQNK.....LSRAADTEEMDIEMDSGDEA 197

Scoring table: BLOSUM62 Gapop 10.0 , Gapext 0.5

747574 seqs, 111073796 residues

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database

| SIBSI/godata/hold-geneseq/geneseqp-embl/AN1980.DNT:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.

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ALIGNMENTS

AAY07107	07107	T LTD
standard;		
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AAY07107;

02-JUL-1999 (first entry)

Colon cancer associated antigen precursor sequence.

prostate cancer Cancer associated antigen: diagnosis; research; treatment; human; breast cancer; colon cancer; gastric cancer; renal cancer; lung cancer;

Homo sapiens

W09904265-A2

15-JUL-1998 28-JAN-1999 98WO-US14679

22-JUN-1998, 17-JUL-1997, 10-OCT-1997, 10-OCT-1997, 10-OCT-1997, 11-OCT-1997, 980S-0102322. 970S-0896164. 970S-0061599. 970S-0061765. 970S-0948705. 97GB-0021697.

(LUDW-) LUDWIG INST CANCER RES

Chen Y, Gout I, Gure A, O'Hare M, (
Pfreundschuh M, Sahin U, Scanlan MJ,
Tureci O; Obata Y, Old LJ; J, Stockert E;

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Matches 197; Conserv
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          06-MAR-1998;
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isolated using sera from cancer patients, used to develop products
for the diagnosis, monitoring or treatment of cancers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 1999-132448/11
                                                            11-SEP-1998
                                                                                                                                                                                     Misc-difference
                                                                                                                                                                                                                                                             Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                        Human secreted protein encoded by gene 106 clone HT3AM65.
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New isolated cancer associated nucleic acids and polypeptides isolated using sera from cancer patients, used to develop products
                                                                                                                                                             WPI; 1999-132448/11
                                                                                                                                 for the diagnosis, monitoring or treatment of cancers
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Disclosure; Page 485-387; 787pp; English.

The Invention relates to a method for disgnosing a disorder that acterised by expression of a human nancer associated antigen precursor coded for by a nucleic scul molecule (NAM). The method comprises: (a) contacting a nucleic scul molecule (NAM). The method comprises: (a) contacting a biological sample isolated from a bubber of that associate that specifically binds to the NAM; an operasion product a fragment of an expression product complexed with an HAM made value or a fragment of an expression product as a fetteraction between the specific has the value as an activity of the characteristic products as the backet as and methods can be used in the disposals, monitoring, teenary furtious center associated antigens that have cancer associated antigen products and encoded polypeptides which are cancer associated antigen products as an activity of the characteristic content of the cancer.

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The present invention provides the protein and coding sequences of a number of human shear stress response proteins. These are useful in the diagnosis, treatment and screening of vascular diseases caused by arteriosclerosis, including heart failure, post-PTCA restenosis and
                                                                                                                                                          DNA sequences, proteins encoded by them and antibodies against them useful in diagnosis and treatment of vascular disease caused by
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                                                                                                  Claim 60; Page 192-195; 678pp; Japanese
                                                                                                                                            arteriosclerosis -
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Total number of hits satisfying chosen parameters: 747574

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Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

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27 / SIDSI/Goddata/hold genesedp-embl/AN19 /SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA1980.DAT:* /SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA1981.DAT:*

Fred, No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

11 11 11	Result No.
4016 3296 2014.5 2009.5 1640.5 1400 896.5 718.5 705.5	Score
91.0 74.7 45.5 45.5 37.2 31.7 20.3 16.3 16.3	Query Match
1068 676 1090 914 914 756 282 1087 1087 388	Query Match Length DB
218222218221	8
AAY59273 AAY59271 AAY59270 AAY59270 AAY59269 AAY59269 AAY59272 AAY59272 AAY59272 AAY59272 AAY59272 AAY59272 AAY59269	ID
Wouse huntingtin-i fuman huntingtin-i fuman huntingtin-i fuman huntingtin-i fuman huntingtin-i wouse huntingtin-i kuman protein sequi Drosophila melanog Drosophila melanog Huntingtin interac Human huntingtin-i	Description

ALIGNMENTS

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Novel proteins useful for treating Huntington		N-PSDB; AAZ58749.	WPI; 2000-097055/08.		t JP, Rasper DM;	Kalchman M. Hayden MR, Hackam A. Chopra V.		(MERI) MERCK FROSST CANADA INC.			27-MAY-1998; 98US-0085199.		27-MAY-1999; 99WO-US11743.		02-DEC-1999.		WO9960986-A2.		Mus sp.		Huntington's disease; nootropic; anticonvulsa	apotosis; HIP-apoptosis modulating protein; c	Huntingtin Interacting Protein; HIP; death ef		Mouse huntingtin-interacting protein (mHIPla)		17-APR-2000 (first entry)		AAY59273;		AAY59273 standard: Protein; 1068 AA.	9273	LT 1

Mouse huntingtin-interacting protein (mHIPla).

Huntingtin Interacting Protein; HIP; death effector domain, DBD; human; apotosis; HIP-apoptosis modulating protein; cell death, gene therapy; Huntington's disease; nootropic, anticonvulsant; cycostatic; mouse.

Kalchman M, Hayden MR, Vallaincourt JP, Rasper Rasper DM; Chopra V, Nicholson

Novel proteins useful for treating Huntington's disease by gene therapy

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Query Match
Best Local S
Matches 801
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The invention relates to Huntingtin Interacting Protein (HIP), that includes a death effector domain (DED), suggesting apototic function. Proteins with DED (referred as HIP-apoptosis modulating proteins) are useful for inducing apoptotic death in cells. The HIP is a logical target for therapy in Huntington's disease since it has a differential apoptotic activity, modulated by interaction with Huntington having normal and expanded repeats. HIP is also used as a therapeutic agent to introduce apoptosis in cancer cells. Increasing expression of normal (one expanded) HUNTINGTON THE HIP-apoptotic modulator binding portion, a modified HIP-apoptotic modulator in which the DED has been deleted, is helpful for
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KYEELIYCSHEIAASTAQLYAASKYKANKHSPHLSRLQECSRTYNERAANYVASTKSGQE 780
                                               \verb|mtstslqkelvesgrgaatqqefyaknsrwtegllsaskavgwgatqlvesadkvvlhmg|
                                                                            TTSTSLQKEIVESGRGAATQQEFYAKNSRWTEGLISASKAVGWGATQLVEAADKVVLHTG 720
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Pred. No. 1.3e-254;
                                                                                                                                                                                                                                                                                       Indels
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215 GELEEQRKQKQKALVDNEQLRHELAQLRAAQLEGERSQGLREEAERKASATEARYNKLKE 274

Matches 674; Query Match Best Local Similarity

Conservative

0;

99.74;

Score 3296; DI Pred. No. 1.1e 0; Mismatches

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Length 676; Indels

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                                The invention relates to Huntingtin interaction, proceeding with public (incition, includes a death effector domain (PE), suggesting process) are useful for inducing appropriate das HIP approasis modulating proteins) are useful for inducing approach dash in peals a might see 109[cal target for therapy in Huntington's disease since it has HIF see 100[cal target activity, modulated by interaction with Huntingtin having normal and expanded repeats. HIP is also used as a therapeuto spent to introduce approach to ancer cells. Increasing expressing formal indeed approach to ancer cells. Increasing expressing obstitute, a modified HIP-apoptocic modulator in which the DED has been deleted; is helpful for the HIP-apoptocic modulator in which the DED has been deleted; is helpful for the HIP-apoptocic modulator.
                                                                                                                                                                                                                                       Claim 3; Page 63-66; 91pp; English
                                                                                                                                                                                                                                                                       techniques, and cancers
                                                                                                                                                                                                                                                                                                                           N-PSDB; AAZ58747
                                                                                                                                                                                                                                                                                                                                                                       Kalchman M, Hayden MR,
Vallaincourt JP, Raspe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Huntingtin Interacting Protein; HTP: death effector domain; DED; human; apotosis; HTP-opoptosis modulating protein; sell death; gene therapy; Huntington's disease; nootropic; anticonvulsant; cytostatic;
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                                                                                                                                                                                                                                                                                   Wovel proteins useful for treating Huntington's disease by
                                                                                                                                                                                                                                                                                                                                                                                                                        (UYBR-) UNIV BRITISH COLUMBIA.

(MERI ) MERCK FROSST CANADA INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         27-MAY-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           02-DEC-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human huntingtin-interacting protein (HIP1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAY59271 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          27-MAY-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens
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GenCore version 4.5 Copyright (c) 1993 - 2000 Comp Compugen Ltd

OM protein - protein search, using sw model

Run on: July 24, 2002, 11:24:45; Search time 95.25 Seconds (Without alignments)
73.171 Willion cell updates/sec

Perfect score: PCT-US02-13994-30 959

Sequence: MQAEGRGTGGSTGDADGPGG... .WITQCFLPVFLAQPPSGQRR 180

Scoring table: Gapop 10.0 , BLOSUM62 Gapext 0.5

105224 seqs, 38719550 residues

Total number of hits satisfying chosen parameters:

Maximum DB seq

Post-processing: Minimum Match length: 2000000000

Maximum Match 100% Listing first 45 summaries SwissProt_40:*

Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

esult		Ouerv					
₹	Score	Match	Length	DB	IĐ	Description	tion
1	959	100.0	180	إ ب	CTAG_HUMAN	P78358	homo sapien
2	595	62.0	210	H	LAG1_HUMAN	63	
w			627	_	HYDL_STRCO	P42534	₽
•	S	16.2	641	_	EBN1_EBV	P03211	epstein-bar
y.	152.5		779	_	CA11_BOVIN	P02453	bos taurus
6	-	15.8	423	_	BR3A_HUMAN	Q01851	homo sapien
7	151.5	15.8	1464	_	CAll_HUMAN	N	homo sapien
B	151	15.7	1901	<u>, , , , , , , , , , , , , , , , , , , </u>	YZOB_MYCTU	053553	mycobacteri
9	148.5	15.5	252	_	GRP1_PHAVU	P10495	phaseolus v
10	148	15.4	1355	-	CA21_RANCA	042350	rana catesb
11	148	15.4	1356	بر.	CA21_ONCMY	093484	oncorhynchu
12	147.5	15.4	1453	μ.	CALL_CHICK	P02457	gallus gall
13	147.5	15.4	1460	. ب	CA11_CANFA	Q9xs 17	canis famil
1	146.5	100	9081		CALB_HUMAN	P12107	nomo sapien
: 5	140	10.2	338	٠,	OKPLAKATH	72/403	arabidopsis
: 5	140.0	7.07	302	٠,	CALB_KAT	606074	ractus norv
		1 .	1001		CC02_CABBL	71000	caenornapur
100	144	15.	421	٠.,	BRAA MOUSE	17208	mus musculus accommendation
20	143.5	15.0	1049	_	CA13_BOVIN	P04258	bos taurus
21	143.5	15.0	1262	_	CA13_CHICK	P12105	gallus gall
22	143	14.9	323	_	YQ34_CAEEL	009455	caenorhabdi
23	142.5	14.9	1466	_	CA13_HUMAN	P02461	homo sapien
24	142	14.8	1372		CA21_MOUSE	001149	mus musculu
25	141.5	14.8	1366	_	CA21_HUMAN	P08123	homo sapien
26	141	14.7	1418	_	CA12_HUMAN	P02458	homo sapien
27	140.5	14.7	671	,_	CA11_RAT	P02454	rattus norv
28	140.5	14.7	1453	,	CALL_MOUSE	P11087	mus musculu
29	140.5	14.7	1603	_	CA1F_HUMAN	007092	homo sapien
30	140	14.6	1459	_	CA12_MOUSE	P28481	mus musculu
31	139.5	14.5	1372		CA21_RAT	P02466	rattus norv
32	139	14.5	375	_	SANT_PLAFY	F09593	plasmodium

45	44	å	2	1	40	39	38	37	36	35	<u>4</u>
136.5	136.5	137	137.5	137.5	137.5	137.5	138	138	138	139	139
14.2	14.2	14.3	14.3	14.3	14.3	14.3	14.4	14.4	14.4	14.5	14.5
1366	1364	3176	3067	1804	108	103	1464	1362	603	1027	747
,_		,	_	_	-	_	-	_	_	-	-
CA21_CANFA	CA21_BOVIN	CA36_HUMAN	CA1C_MOUSE	CALB_MOUSE	Y747_HYCTU	YDH3_HSVSC	CA13_MOUSE	CA21_CHICK	YD25_MYCTU	CAFF_RIFPA	CA12_BOVIN
	P02465 bos taurus										

ALIGNMENTS

RESU	RESULT 1		
CTAG	CTAG_HUMAN		
Ū	CTAG_HUMAN	STANDARD; PRT; 180 AA.	•
ð	P78358;		
7	15-DEC-1998	(Rel. 37, Created)	
Ď,	15-DEC-1998	<pre>15-DEC-1998 (Rel. 37, Last sequence update)</pre>	
2	16-OCT-2001	(Rel. 40, Last annotation updat	e)
DE	Autoimmunoge	nic cancer/testis antigen NY-ES	0-1.
2			

Homo sapiens (Human). Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidee; Homo.

SEQUENCE FROM N.A. NCBI_TaxID-9606;

MEDILNE-97203161, PubMed-9508099;
Chen K.-T., Scanlan M.J., Sahln Di,, Tuereci O., Gure A.O., Tsang S.,
Williamson B., Stockert E., Pfreundschuh M., Old L.J.;
*A teasticular antigen aberrantly expressed in human cancers detected
by autologous antibody screening*, expression of the control o

SEQUENCE FROM N.A.

TISSUE-Melanoma

MEDLINE-98289662; PubMed-9626360;

Lethe B., Lucas S., Michaux L., de Smet C., Godelaine D., Serrano A., de Plaen E., Boon T.;
LAGE-1 a new gene with tumor specificity.;
Int. J. Cancer 76:903-908(1998).

SEQUENCE FROM N.A.

PRESENTATION OF A PRESENTATION MEDIANE-98430682; PubMed-995882;
MADDER F. LONDARDO S.L., Zeng G., Topalian S.L.,
Schwartzentruber D.J., Bosenberg S.A.;
*A breast and melanoma-shared tumor antigen: T cell responses to
antigenic paptides translated from different open reading frames.*;
J. TISSUB-SPECIFICITY: BYANGES IN TESTIS AND OVARY AND IN A WIDE
1- TISSUB-SPECIFICITY: STANGES DETECTED IN OTERINE MICHERIUM.
1- STANLENT OF CANCERS. DETECTED IN OTERINE MICHERIUM.

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EMBL; U87459; AAB49693.1; -. EMBL; AJ003149; CAA05908.1; -. EMBL; AF038567; AAD05202.1; -.

мім; 300156; -

Transmembrane; Antigen. 5 82 6 172 POTENTIAL

TRANSMEM

33

139

14.5

463

YA68_MYCTU

053416 mycobacteri

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Best Local Sim
Matches 180;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LAG1_HUMAN STANDARI
O7563B; O75637;
30-MAY-2000 (Rel. 39, 0
30-MAY-2000 (Rel. 39, 1
16-CCT-2001 (Rel. 40, 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LHUMAN
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                                                                                                                                                                      EMBL; AJ223093; CAA11116.1; -
EMBL; AJ223040; CAA11043.1; -
EMBL; AJ223041; CAA11044.1; -
                                                                                                                                                                                                                                                              This SMISS-PROY entry is copyright. It is produced through a collaboration between the SWHS institute of Bioinformatics and the EMBL outstation the European Bioinformatics institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                           Polymorphism: Alternative DOMAIN 5 79 DOMAIN 183 188 VARSPLIC 135 210
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                 VARIANT
                                                VARIANT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens (Human)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 MQAEGRGTGGSTGDADGPGGPGIPDGPGGNAGGPGEAGATGGRGPRGAGAARASGPGGGA 60
                                                                                                                                                                                                                                                                                                                                                                                                       HERRE); ARE PRODUCED BY ALTERNATIVE SPLICING.
TISSUE SPECIFICITY: TESTIS AND VERY LOW LEVEL IN PLACENTA AND
SOME UTENS SAMPLES, OBSERVED IN 25-504 OF TUMOR SAMPLES OF
MELANOMAS; NON-SMALL-CELL LUNG CARCINOMAS, BLADDER, PROSTATE &
HEAD AND NECK CANCERS.
                                                                                                                                                                                                                                                                                                                                                                          DOMAIN: A TRANSMEMBRANE DOMAIN IS PRESENT IN ISOFORM LAGE-1A SIMILARITY: STRONG, TO NY-ESO-1/CTAG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ALTERNATIVE PRODUCTS: 2 ISOFORMS; LAGE-1A AND LAGE-1B
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                                                                                                                                                                                                                     AJ223093; CAA11117.1; -.

    a new gene with tumor specificity.",
Cancer 76:903-908(1998).

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                   89
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                                                                                                                                                       splicing; Transmembrane; Antigen
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                                                         POLY-PO.

KSYMOODREGAGHRYVGWGLGSASPEGGKARDLRTPKHKY
SEQREGTFGPPPPEGAGGGCGGVARWAFSARHI -> IR
LTAADHROLGGISIGCIQALKHTYVAFSARHI -> IR
LTAADHROLGGISIGCIQALKHTYQFFPVFLAQARSG
QRR (IN ISOFOOM LAGE-IA).
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Pred. No. 5.4e-61;
                 /FTId-VAR_007855
E -> Q.
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Best Local
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HYDL_STRCO STAN

P42534; Q9S2L7;

01-NOV-1995 (Rel. 1

16-OCT-2001 (Rel. 1

16-OCT-2001 (Rel. 1
                                                                                                                                                                                                                                                                                                          Blanco C., Pereda A., Brian P., Mendez C., Chater K.F., Salas J.A.;
*A hydroxylase-like gene product contributes to synthesis of a
polyketide spore pigment in Streptomyces halstedil.';
J. Bacteriol. 175:8043-8048(1993).
1- EUNCTION. INVOLVED IN DEVELOPMENTALLY REGULATED SYNTHESIS OF A
COMPOUND BIOSYNTHETICALLY RELATED TO POLYKETIDE ANTIBIOTICS,
WHICH LS ESSENTIAL DOR SPORE COLOR IN STREPTOCOCCUS COELICOLOR.
1- COPACTOR: PAD (BY SIMILARITY)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     16-0CT-2001 (Rel. 40, Last sequence update)
16-0CT-2001 (Rel. 40, Last annotation update)
Putative polyketide hydroxylase (EC 1.14.13.) (WhiE ORF VIII).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VARIANT
                                                                                                                                                                                               This SMISS-PROT entry is copyright. It is produced through a collaboration between the Swiss institute of Bioinformatics and the BMB outstation on the BMB outstation on the buropean Bioinformatics institute, There are no restrictions on the modified and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Seeger K.J., Harris D., James K.D., Rajandream M.A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE
Oxidoreductase: Flavoprotein: FAD. NP_BIND 22 51 FAD. NP_BIND 309 319 FAD.
                                                         EMBL: AL079356: CR8456031: --
EMBL: X74213: CAA52289.1:
InterPro: IPR000087: Collagen.
InterPro: IPR002938: Moxy_FAD_binding
InterPro: IPR002942: Roz_moxygenase.
Pfam; PF01494; FAD_binding_3; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Actinomycetales;
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                                           PRINTS; PRO0420; RNGMNOXGNASE
                                                                                                                                                                    entities requires a license agreement (See http://www.isb-sib.ch/announce/
or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE-94075247; PubMed-8253693;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE OF 1-255 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=1902;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                             SIMILARITY: BELONGS TO THE PHEA/TFDB FAMILY OF FAD MONOOXYGENASES
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Pred. No. 1
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FAD (POTENTIAL).
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GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

July 24, 2002, 11:17:18; Search time 197.76 Seconds
91.347 Million cell updates/sec

Run on:

Sequence: Title: Perfect score: PCT-US02-13994-28 1012 MNGDDAFARRPTVGAQIPEK.....RERKQLVIYEEISDPEEDDE 188

Scoring table: Gapop 10.0 , Gapext 0.5

Total number of hits satisfying chosen parameters: 283138 seqs, 96089334 residues

283138

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database : PIR_71:* pir2: pir3: pir4: pir1:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

27 85	25 85 26 85	8 6 5 5	17 87 18 87 19 86.5 20 86	14 87.5 15 87.5 16 87.5	11 88.5 12 88 13 87.5	7 91.5 8 91.5 9 90.5 10 88.5	1 1012 2 772 3 107 4 101 5 99	Result
B .↓	2000	999	B B B B		8.7 8.7	8.9 9.0 8.7	100.0 76.3 10.6 9.8 9.3	Query
1167 75 5	210 210 1162	990 2251 2270	346 1559 654 1087	209 541 586	270 445 186	252 1507 1153 213	188 188 1111 289 392 952	Length
~ ~	NNN		- 2 2 2	221	ผผผ	พพพพ	анинин	D B
A35066	A34/19 S54774 T51040	IS1618 B54972 A54972	C88961 T30535 A57785 QFMSH	NSHUH2 T48836 B84434	188734 123908 830221	T20321 B47328 T21386 JQ0075	\$55058 \$55057 \$100324 \$140913 \$119327 \$64473	SUMMARIES
streptococcal C5a filensin - bovine	nonhistone chromos high mobility grou hypothetical prote	nucleolar phosphop voltage-dependent voltage-dependent	<pre>protein F59A7.5 [i calcium channel al finger protein ZNF neurofilament trip</pre>	nonhistone chromos hypothetical prote hypothetical prote	<pre>protein F32E10.2 [hypothetical prote nonhistone chromos</pre>	hypothetical prote natural killer cel hypothetical prote neuromodulin - gol	synovial sarcoma X SSXI protein - hum hypothetical prote KRAB zinc finger p hypothetical prote translation initia	Description

hypothetical prote	T15662	N	279	8.1	82	45
hypothetical prote	T21068	N	279	8.1	82	44
nuclear antigen EB	827922	N	1069	8.2	82.5	3
gene 11-1 protein	S00485	N	1948	8.2	8.3	42
SARA protein - Afr	T17457	N	1235	8 .2	83	1
NF-180 - sea lampr	151116	N	1110	8 .2	83	0
Inv protein - mous	T14151	N	1062	8.2	83	39
hypothetical prote	F84514	N	783	8.2	83	8
l-afadin - rat	T41751	N	1829	8.3	83.5	37
s-afadin - rat	T42092	N	1663	8.3	83.5	36
DNA topoisomerase	A39242	N	1626	8.3	83.5	35
hypothetical prote	100365	N	1280	8	83.5	34
dynamin-like prote	T52426	N	920	8.	83.5	33
gene NK10 protein	I48689	N	636	8.3	83.5	32
proline-rich prote	E29149	N	301	8.3	83.5	31
SNF2beta protein .	S45252	N	1647		84	30

ALIGNMENTS

synovial sarcoma x chromosome breakpoint protein SSX2 - human
Cispacies: Abnob saptens (man)
Cispacie: 28-oct 1996 #sequence revision 13-Mar-1997 #text_change 01-Dec-2000
Ciaccession: SS5058; Ide675: S4573
Ciaccession: SS5058; Ide675: S4573
RCICHA, J. Fisher, C.; Gill, S.; Grimer, R.; Chand, A.; Shipley, J.; Gu
BMDO: 14, 2333-2340, 1995 Sher, C.; Gill, S.; Grimer, R.; Chand, A.; Shipley, J.; Gu
A; Title: Fasion of STT to two genes, SSX1 and SSX2, encoding proteins with homology t
A; Reference number: SS557; MUID: SS292374
A; Accession: SS5058

A;Status: preliminary A;Molecule type: mRNA A;Residues: 1-188 <CRE>

A:Gross:references: EMBL:X86175; NID:g823113; PIDN:CAA60111.1; PID:g4218445
R:d6 Lecuty B.; Balemans, H.; Olde Sephuis, D.; Geurts van Kessel, A.
Hum. Hol. Genet, 4. 1097-1099, 198
A:Title: Identification of two alternative fusion genes, SYT-SSX1 and SYT-SSX2, in t(A:Reference number: IS4381; MUID:95384157
A:Accession: I68675

A;Status: preliminary; translated from GB/EMBL/DDBJ A;Molecule type: mRNA A;Residues: 111-188 <RES>

A;Cross-references: Gb:S79332; NID:q1087049; PIDN:AAB35379.1; PID:q1087050 R;Clark, J.; Rocques, P.J.; Grew, A.J.; Gill, S.; Shipley, J.; Chan, A.H.L.; Gusterso Mature Genet., J.; 502-508, 1994

A.Title: Identification of novel genes, SYT and SSX, involved in the t(X:18) (p11.2:q A:Reference number: \$46269; MUID:95038836 A:Accession: \$46270

A; Molecule type: mRNA A; Residues: 111-188 <CLA> A; Cross-references: EMBL: X79200

A; Gene: SYT-SSX2

ş В Q 용 Q Ouery Match 100.0%; Score 1012; DB 2; Best Local Similarity 100.0%; Pred, No. 1.8e-78; Matches 188; Conservative 0; Mismatches 0; 121 NDSEEVPEASGPQNDGKELCPPGKPTTSEKIHERSGPKRGEHAWTHRLRERKQLVIYEEI 180 61 61 1 MNGDDAFARRPTVGAQIPEKIQKAFDDIAKYFSKEEWEKMKASEKIFYVYMKRKYEAMTK 60 LGFKATLPPFMCNKRAEDFOGNDLDNDPNRGNQVERPOMTFGRLQGISPKIMPKKPAEEG 120 MNGDDAFARRPTVGAQIPEKIQKAFDDIAKYFSKEEWEKNKASEKIFYVYMKRKYEAMTK 60 LGFKATLPPFHCNKRAEDFQGNDLDNDPNRGNQVERPQNTFGRLQGISPKIMPKKPAEEG 120 Indels Length 188; 0 Gaps 0

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hypothetical protein KLAA0543 - human (fragment)
Cispecies: Homo aaplens (man)
Cipate: 01-Feb-1999 #sequence_revision 01-Feb-1999 #text_change 21-Jul-2000
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R:de Leeuw, B.; Balemans, M.; Olde Weghnis, D.; Geutts van Kessel, A.
Hum. Mol. Genet. 4, 1097-1099, 1995
A:Title: Identification of two alternative fusion genes, SYT-SSX1 and SYT-SSX2, in t(X: A:Reference number: 154381; MVID:95384157
A:Accession: 154381
                                                                                                                                      A:Status: preliminary; translated from GB/EMBL/DDBJ
A:Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: mRNA
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A:Molecule type: mRNA
A:Status: preliminary; translated from GB/EMBL/DDBJ
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A;Molecule type: mRNA
A;Residues: 111-188 <RES>
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A; Residues: 1-188 < CRE>
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                                                                                                                       A; Experimental source: brain
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Best Local
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nes 147; Conserv
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                                                      KIAA0543
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78.21;
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Pred. No. 3.5e-58;
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A:Cross-references: GDB:131
A:Knap position: Xq26-Xq26
A:Introns: 11/3
C:Reywords: zinc finger
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A; Residues: 139-289 <MAR>
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                                                                17 IPEKIQ-KAPDDIAKYESKEEWEKMKASEKIFY-VYMKRKYEAMTKLGEKATLPPFMCNK 74
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A:Status: preliminary
A:Status: preliminary
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A:Residues: 71-289 </TI.>
A:Residues: 71-289 </TI.
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C:Species: Homo sapiens (man)
C;Date: 10-May-1996 #sequence_revision 10-May-1996 #text_change 05-Nov-1999
C;Dates: 10-May-1996 #sequence_revision 10-May-1996 #text_change 05-Nov-1999
C;Accession: A48913; A4288; $47339
R:Villa, A.; Zucchi, I.; Patrosso, C.;
Genomics 18, 223-229, 1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A:Cross-references: GB:565/970, MD:9460902; PIDM:AAB29696.1; PID:9460903
A:Experimental gource: Ing fibrobleats
R:Villa, A.; Patrosso, C.; Blunno, I.; Frattini, A.; Repetto, H.; Mostardini,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A.Title: ZNF75: isolation of a cDNA clone of the KRAB zinc finger gene subfamily mapp
A.Reference number: A48913; MUID:94116987
A.Accession: A48913
                                                                                                                   A;Cross-references: EMBL:X68010; NID:g525243; PIDN:CAA48147.1; PID:g525244
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GDB:131726; OMIM:31499;
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MAGA_HUMAN
MAGB_HUMAN
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P07101 homo sapien	TY3H_HUMAN	_	528	5.	88.5	ū
Q25410 lympaea sta	MIPR_LYMST	_	1607	5.4	89	2
013428 homo sapien	TCOF_HUMAN	_	1411	٠.	89	Ξ
007017 streptomyce	OL56_STRAT	_	3519	.5	89.5	ō
P49083 OTYZA Sativ	GBA1_ORYSA	-	380	5.6	91	9
Q9y603 homo sapien	TEL2_HUMAN	_	341	5.6	16	ă
007345 synechococc	CHLD_SYNP7	_	677	5	91.5	7
099575 homo sapien	POP1_HUMAN	-	1024	6	92	6
096018 homo sapien	APB3_HUMAN	,_	575	5.6	92	ŭ
P25365 saccharomyc	SED4_YEAST	_	1065	5.7	93	-

MAG3_HUMAN P43357; 01-NOV-1995 (Rel. 32, Created) 01-NOV-1995 (Rel. 32, Last Septence update) 01-MAR-2002 (Rel. 41, Last annotation update) Melanoma-associated antigen 3 (MAGE-3 antigen) (Antigen M22-D) MAGEA3 OR MAGE3. HUMAN STANDARD; ζ

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammaila; Eutheria; Primates; Catarrhini; Hominidae; Homo.

NCBI_TaxID-9606; Homo sapiens (Human)

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KEDLINE-20314695; PubMed-10854409;
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SEQUENCE FROM N.A.

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WEDLINE-95012457: PubHed-7927540; de Plaen E., Arden K., Traversari C., Gaforio J.J., Szikora J.-P., de Plaen E., Arden K., Traversari C., Gaforio J.J., Szikora J.-P., de Baseu C., Basseu F., van der Brugges P., Lethe B., Lurquin C., Brassour R., Chomez P., de Backer O., Cavence W., Appression of 12 genes o Structure, chromosomal localization, and expression of 12 genes o
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Eukaryota; Metazoa; C
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D->A: ABOLISHES HLA-A1 BINDING.
Y->A: ABOLISHES HLA-A1 BINDING.
Y->A: ABOLISHES HLA-A1 BINDING.
; 3F5EB13D1C9946A1 CRC64;
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0; Mismatches
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PPQSPQGASSLPTTMNYPLWSQSYEDSSNQEEEGPSTFPDLESEFQAALSRKVAKLVHFL

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Query Match Best Local S Matches 301

Local Similarity

95.98;

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DPKKLLTQYFVQENYLEYRQVPGSDPACYEFLWGPRALIETSYVKVLHHMVKISGGPRIS DPKKLLTQHFVQENYLEYRQVPGSDPACYEFLWGPRALVETSYVKVLHHWVKISGGPHIS

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the MAGE family
Immunogenetics 4
[2]
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"Sequence analysis of the MAGE gene family encoding human tumor rejection antiquess";
Gone 160-007
                                                                                                                                                                                                                                                                                                                                                                This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss institute out fluor can add the DMH outstation the European Bloinformatics size in formatics and the DMH outstation is burneyed. The control of the contr
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Ding M., Beck R.J., Keller C.J., Fenton R.G.;
Cloning and analysis of MAGE-1-related genes. ;
Blochem. Blophys. Res. Commun. 202:549-555(1994).
DOMAIN
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
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                                                         PROSITE: PS50838; MAGE: 1
Antigen: Multigene family,
DOMAIN 109 308
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gene 160
                                                                                                                                                                                                                   MIM;
                                                                                                                                                                                    InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MAGE family.";
unogenetics 40:360-369(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PUNCTION: NOT KNOWN, THOUGH MAY PLAY A ROLE IN TUMOR OR ASPECT, OF TUMOR PROGRESSION.
TISSUE SPECIFICITY: EXPRESSED IN MANY TUMORS OF SEVERAL TYPES, OUTH AS MELANOMA, HAD AND MECK SQUAMOUS CELL CARCIMOMA, LUMC CARCIMOMA BREAST CHREINOMA, BUT NOT IN NORMAL TISSUES EXCEPT CARCIMOMA, BUT NOT IN NORMAL TISSUES EXCEPT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FUNCTION: NOT KNOW
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                                                                                                                                                                                                                   300176;
                                                                                                                                                                                                                                                  U10691; AAA68875.1; -. U10339; AAA19006.1; -. D32076; BAA06842.1; -.
                                                                                                                                                          PF01454; MAGE;
                                                                                                                                                                                        IPR002190; MAGE
        314 AA;
                                       ô
                                                             e family: Tumor antigen
        34891 MW;
    POLY-SER.
; 29883C7FA6E50263 CRC64
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